

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 23, 2003, 18:00:50 : Search time 25.7561 Seconds
(without alignments)
1149.607 Million cell updates/sec

Title: US-10-088-548-2

Perfect score: 1786

Sequence: 1 KSPVQDCYHGDGRSYRGIS.....YTMNPKLFDYCDPLCASS 308

Scoring table: BIOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :
1: PIR_73:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1780	99.7	4548 1	apoprotein(a) (EC 3.4.21.1) precursor [validated] - human
2	1210.5	67.8	810 1	plasma (EC 3.4.21.1) precursor [validated] - human
3	1205.5	67.5	810 2	plasma (EC 3.4.21.1) precursor [validated] - human
4	1195.5	66.9	1420 2	apoprotein(a) (EC 3.4.21.1) precursor [validated] - human
5	1137.5	63.7	812 1	plasma (EC 3.4.21.1) precursor [validated] - human
6	1124	62.9	790 1	plasma (EC 3.4.21.1) precursor [validated] - human
7	1123.5	62.9	812 1	plasma (EC 3.4.21.1) precursor [validated] - human
8	1072	60.0	810 2	plasma (EC 3.4.21.1) precursor [validated] - human
9	808.5	45.3	460 2	plasma (EC 3.4.21.1) precursor [validated] - human
10	796	44.6	2869 2	plasma (EC 3.4.21.1) precursor [validated] - human
11	787.5	44.1	455 2	plasma (EC 3.4.21.1) precursor [validated] - human
12	685.5	38.4	728 1	hepatocyte growth factor (EC 3.4.21.1) precursor [validated] - human
13	685.5	38.4	728 1	hepatocyte growth factor (EC 3.4.21.1) precursor [validated] - human
14	680.5	38.1	728 1	hepatocyte growth factor (EC 3.4.21.1) precursor [validated] - human
15	671	37.6	711 1	hepatocyte growth factor (EC 3.4.21.1) precursor [validated] - human
16	670.5	37.5	716 1	hepatocyte growth factor (EC 3.4.21.1) precursor [validated] - human
17	656	36.7	710 1	hepatocyte growth factor (EC 3.4.21.1) precursor [validated] - human
18	650.5	36.4	716 1	hepatocyte growth factor (EC 3.4.21.1) precursor [validated] - human
19	620	34.7	169 2	hepatocyte growth factor (EC 3.4.21.1) precursor [validated] - human
20	604.5	33.8	411 2	hepatocyte growth factor (EC 3.4.21.1) precursor [validated] - human
21	413	23.1	120 2	hepatocyte growth factor (EC 3.4.21.1) precursor [validated] - human
22	408	22.8	123 2	hepatocyte growth factor (EC 3.4.21.1) precursor [validated] - human
23	390	21.8	336 2	hepatocyte growth factor (EC 3.4.21.1) precursor [validated] - human
24	387	21.7	622 2	hepatocyte growth factor (EC 3.4.21.1) precursor [validated] - human
25	363.5	20.4	625 2	hepatocyte growth factor (EC 3.4.21.1) precursor [validated] - human
26	354	19.8	89 2	hepatocyte growth factor (EC 3.4.21.1) precursor [validated] - human
27	352.5	19.7	618 2	hepatocyte growth factor (EC 3.4.21.1) precursor [validated] - human
28	338.5	19.0	617 2	hepatocyte growth factor (EC 3.4.21.1) precursor [validated] - human
29	338	18.9	562 1	hepatocyte growth factor (EC 3.4.21.1) precursor [validated] - human

ALIGNMENTS

30	301.5	16.9	559 1	A29941	t-plasminogen acti
31	298.5	16.7	559 1	A35029	t-plasminogen acti
32	271.5	15.2	946 1	A47299	ror-related recep
33	257.5	14.4	943 2	B45082	neurotrophic recep
34	246.5	13.8	291 2	I38098	t-plasminogen acti
35	241	13.5	615 1	KFH012	coagulation factor
36	240.5	13.5	603 2	S28941	coagulation factor
37	225	12.6	655 1	A46688	hepatocyte growth
38	223.5	12.5	560 1	JC4795	plasma hyaluronan-
39	223.5	12.5	593 2	S45281	coagulation factor
40	213.5	12.0	937 2	A45082	neurotrophic recep
41	208	11.6	558 2	JCS878	plasma hyaluronan-
42	180.5	10.1	442 1	UK86	u-plasminogen acti
43	179.5	10.1	433 1	JN0560	u-plasminogen acti
44	179	10.0	432 1	S18932	u-plasminogen acti
45	173.5	9.7	433 1	UK86	u-plasminogen acti

RESULT 1
S00657
apoprotein(a) (EC 3.4.21.1) precursor [validated] - human
N:Alternate names: apolipoprotein(a); lipoprotein(a) chain apo(a)
C:Species: Homo sapiens (man)
C>Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 08-Dec-2000
C:Accession: S00657; A28017; A47277; I60906; A47233; I52415; I65286
R:McLean, J.W.; Tomlinson, J.E.; Kuang, W.J.; Eaton, D.L.; Chen, E.Y.; Fless, G.M.; Nature 330, 132-137, 1987
A>Title: CDNA sequence of human apolipoprotein(a) is homologous to plasminogen.
A:Reference number: S00657; MID:88039109; PMID:3670400
A:Accession: S00657
A:Molecule type: mRNA
A:Residues: 1-4548 <MCL>
A:Cross-references: GB:X06696; EMBL:X06696; NID:928619; PIDN:CA29618.1; PID:928620
R:Eaton, D.L.; Fless, G.M.; Kohr, W.J.; McLean, J.W.; Xu, Q.T.; Miller, C.G.; Lam, Proc. Natl. Acad. Sci. U.S.A. 84, 3224-3228, 1987
A>Title: Partial amino acid sequence of apolipoprotein(a) shows that it is homologous
A:Reference number: A28017; MID:87204109; PMID:3472206
A:Accession: A28017
A:Molecule type: protein
A:Residues: 20-21, 'P', '23-34; 177-179, 'N', '181-186, 'T', '188-196, 'DKG', '200; 292-314, 'W', '31
X', '4396-4401 <EAT>
R:Wade, D.P.; Clarke, J.G.; Lindahl, G.E.; Liu, A.C.; Zysow, B.R.; Meier, K.; Schwartz Proc. Natl. Acad. Sci. U.S.A. 90, 1369-1373, 1993
A>Title: 5' control regions of the apolipoprotein(a) gene and members of the related
A:Reference number: A47277; MID:93165698; PMID:7679504
A:Accession: A47277
A>Status: preliminary; translation not shown; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-16 <RES>
A:Cross-references: GB:L07899; NID:9667973; PID:9667974
R:Magarelli, N.; Acquati, F.; Magnaghi, P.; Bruno, L.; Pontoglio, M.; Rocchi, M.; S Proc. Natl. Acad. Sci. U.S.A. 89, 11584-11588, 1992
A>Title: Characterization by yeast artificial chromosome cloning of the linked apoli
A:Reference number: A47233; MID:93087573; PMID:1454851
A:Accession: I60906
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-16 <RE2>
A:Cross-references: GB:M90078; NID:9178786; PIDN:AAA35547.1; PID:9553188
A>Note: apo(a) gene 1 (nomenclature of reference I52415)
A:Accession: A47233
A>Status: preliminary; translation not shown; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-16 <RE5>
A:Cross-references: GB:M90079; NID:9178784; PIDN:AAA35546.1; PID:9553187
R:Richiense, A.
Biochemistry 31, 3113-3118, 1992
A>Title: Multiple members of the plasminogen-apolipoprotein(a) gene family associate
A:Reference number: I52415; MID:92207924; PMID:1554698
A:Accession: I52415

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 116 <RB3>
A:Cross-references: GB:M86877; NID:q178780; PIDN:AA849909.1; PID:9553185
A:Note: apo(a) gene 1 (nomenclature of reference I52415)
A:Accession: 165286
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 116 <RB4>
A:Cross-references: GB:M86878; NID:q178782; PIDN:AA51749.1; PID:9553186
C:Genetics:
A:Gene: GDB:LPA
A:Cross-references: GDB:120699; OMIM:152200
A:Map position: 6q26-6q27
A:Note: several genes closely linked on chromosome 6 are identical in the first coding
rs of kringle repeats
C:Superfamily: apolipoprotein(a); kringle homology; trypsin homology
C:Keywords: hydrolase; kringle; lipid binding; lipoprotein; serine proteinase
F:1.19/Domain: signal sequence #status predicted <SIC>
F:20-4548/Product: apolipoprotein(a) #status experimental <MAT>
F:28-105/Domain: kringle homology <KR1>
F:142-219/Domain: kringle homology <KR2>
F:256-333/Domain: kringle homology <KR3>
F:370-447/Domain: kringle homology <KR4>
F:484-561/Domain: kringle homology <KR5>
F:598-675/Domain: kringle homology <KR6>
F:712-789/Domain: kringle homology <KR7>
F:826-903/Domain: kringle homology <KR8>
F:940-1011/Domain: kringle homology <KR9>
F:1054-1131/Domain: kringle homology <KR10>
F:1168-1245/Domain: kringle homology <KR11>
F:1282-1359/Domain: kringle homology <KR12>
F:1396-1473/Domain: kringle homology <KR13>
F:1510-1587/Domain: kringle homology <KR14>
F:1624-1701/Domain: kringle homology <KR15>
F:1738-1815/Domain: kringle homology <KR16>
F:1852-1929/Domain: kringle homology <KR17>
F:1966-2043/Domain: kringle homology <KR18>
F:2080-2157/Domain: kringle homology <KR19>
F:2194-2271/Domain: kringle homology <KR20>
F:2308-2385/Domain: kringle homology <KR21>
F:2422-2499/Domain: kringle homology <KR22>
F:2536-2613/Domain: kringle homology <KR23>
F:2650-2727/Domain: kringle homology <KR24>
F:2764-2841/Domain: kringle homology <KR25>
F:2878-2955/Domain: kringle homology <KR26>
F:2992-3069/Domain: kringle homology <KR27>
F:3106-3183/Domain: kringle homology <KR28>
F:3220-3297/Domain: kringle homology <KR29>
F:3334-3411/Domain: kringle homology <KR30>
F:3448-3525/Domain: kringle homology <KR31>
F:3562-3639/Domain: kringle homology <KR32>
F:3676-3753/Domain: kringle homology <KR33>
F:3782-3859/Domain: kringle homology <KR34>
F:3896-3973/Domain: kringle homology <KR35>
F:4010-4087/Domain: kringle homology <KR36>
F:4124-4201/Domain: kringle homology <KR37>
F:4228-4307/Domain: kringle homology <KR38>
F:4328-4541/Domain: trypsin homology <TRY>

Query Match 99.7%; Score 1780; DB 1; Length 4548;
Best Local Similarity 99.7%; Pred. No. 2, 6e-123;
Matches 307; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
IV37

DB 4123 OCYHNGOSYRGTFSTVTGRTGOSWSSMTPHRRORFENYNDGLTFMNYCRNPDAOTGP 4182
QY 181 WFTTDPSTRMEXCNLTGSCSTEGTVAPPTVIOYPSISGPFSEDDCFNGKRGKAT 240
DB 4183 WFTTDPSTRMEXCNLTGSCSTEGTVAPPTVIOYPSISGPFSEDDCFNGKRGKAT 4242
QY 241 TVTGTPOEWAQOEPRHSTFIPGTNKWAGLEKNCRNPDGDINGPCCYTNPKRLDYC 300
DB 4243 TVTGTPOEWAQOEPRHSTFIPGTNKWAGLEKNCRNPDGDINGPCCYTNPKRLDYC 4302
QY 301 DIPLCASS 308
DB 4303 DIPLCASS 4310
V38

RESULT 2
PHTU
plasmin (EC 3.4.21.7) precursor [validated] - human
N:Alternate names: plasminogen precursor [misnomer]
N:Contains: angiotatin; microplasmin; plasminogen
C:Species: Homo sapiens (man)
C:Date: 24-Apr-1984 #sequence revision 02-Dec-1994 #text change 15-Sep-2000
C:Accession: A35229; I52242; A26646; I62738; I84609; S03735; A00929; A04627; A04625;
R:Peterson, T.E.; Maitzen, M.R.; Ichinose, A.; Davie, E.W.
J. Biol. Chem. 265, 6104-6111, 1990
A:Title: Characterization of the gene for human plasminogen, a key proenzyme in the f
A:Reference number: A35229; MUID:90202879; PMID:2318848
A:Accession: A35229
A:Molecule type: DNA
A:Residues: 1810 <PEP>
A:Cross-references: GB:J05286; GB:M34276; NID:q190064; PIDN:AAA60113.1; PID:9387026
A:Experimental source: leukocyte; lung fibroblast
R:Margaret, N.; Bruno, L.; Pontoglio, M.; Candiani, G.; Meroni, G.; Ottolenghi, S.;
Biochem. Biophys. Res. Commun. 173, 1013-1018, 1990
A:Title: Definition of the transcription initiation site of human plasminogen gene in
A:Reference number: I52242; MUID:1095523; PMID:2268308
A:Accession: I52242
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-16 <MAL1>
A:Cross-references: GB:M62890; NID:q190092; PIDN:AAA34654.1; PID:9553613
R:Forsgren, M.; Raden, B.; Israelsson, M.; Larsson, K.; Heden, L.O.
FEBS Lett. 213, 254-260, 1987
A:Title: Molecular cloning and characterization of a full-length cDNA clone for human
A:Reference number: A26646; MUID:87162490; PMID:3030813
A:Accession: A26646
A:Molecule type: mRNA
A:Residues: 1-471, 'D', 473-810 <FOR>
A:Cross-references: GB:X05199; NID:q35530; PIDN:CAA28831.1; PID:935531
A:Experimental source: liver
R:Malinowski, D.P.; Sadler, J.E.; Davie, E.W.
Biochemistry 23, 4243-4250, 1984
A:Title: Characterization of a complementary deoxyribonucleic acid coding for human a
A:Reference number: I45961; MUID:85023311; PMID:6148961
A:Accession: I45961
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 292-471, 'D', 473-810 <MAL2>
A:Cross-references: GB:K02922; NID:q190112; PIDN:AAA60124.1; PID:9387031.
A:Accession: I84609
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 367-419 <MAL3>
A:Cross-references: GB:K02921; NID:q190110; PIDN:AAA60123.1; PID:9190111
R:Brundholz, R.A.; Lerch, P.G.; Schaller, J.; Rickli, E.E.; Lergler, W.; Manneberg,
Eur. J. Biochem. 114, 465-470, 1981
A:Title: Comparison of the primary structure of the N-terminal CNBr fragments of huma
A:Reference number: S03735; MUID:81212097; PMID:7238497
A:Accession: S03735
A:Molecule type: protein
A:Residues: 20-71, 'E', 73-76 <BRU>
R:Sottirup-Jensen, L.; Petersen, T.E.; Magnusson, S.